

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2003, 14:23:37 ; Search time 3958 Seconds
(without alignments)
16051.706 Million cell updates/sec

Title: US-09-745-506-74

Perfect score: 1553
Sequence: 1 GTGATTGTATCTTGCTGCT.....TCTGTACTTAACATTCMA 1553

Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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1: gb_da:*
2: gb_htg:*
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41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	1138	73.3	1440	9	BC007654
6	1137	73.2	1387	9	AF060513
7	1053	67.8	1053	6	AX119075
8	1027	66.1	1353	9	HSMB05522
9	852	54.9	1579	9	AF182416
10	567	36.5	796	6	BD149184
11	414	26.7	170586	2	AC037455
12	414	26.7	190508	9	AC005037
13	414	26.7	198250	2	AC093681
14	210	13.5	249	6	BD049005
15	141	9.1	198250	2	AC093681
16	90	5.8	339	6	BD040994
17	50	3.2	55374	9	AL645474
18	41	2.6	131	6	BD037535
19	38	2.4	1836	10	AF284439
20	38	2.4	149819	2	AC121091
21	38	2.4	231600	2	AC130779
22	38	2.4	234976	2	AC118698
23	22	1.4	11976	6	AX345497
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28	21	1.4	102223	9	AC022432
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ALIGNMENTS

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LOCUS
DESTINATION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

BD158389
BD158389
BD158389
JP 2002191363-A/13232.
Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1574)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof

Pred. No. is the number of results predicted by chance to have a

TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS 1606 bp mRNA linear PRI 23-FEB-2001
DEFINITION Homo sapiens AHS2CR1 mRNA for amyotrophic lateral sclerosis 2,
candidate 1, complete cds.
VERSION
AB038949
AB038949.1 GI:12862477
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (sites)
Hadano,S., Yanagisawa,Y., Skaug,J., Fliciter,K., Nasir,J.,

TITLE

Martindale, D., Koop, B.F., Scherer, S.W., Nicholson, D.W., Rouleau, G.A., Ikeda, J.-E. and Hayden, M.R. Cloning and characterization of three novel genes, *ALS2CR1*, *ALS2CR2*, and *ALS2CR3*, in the juvenile amyotrophic lateral sclerosis (*ALS2*) critical region at chromosome 2q33-q34: candidate genes for *ALS2*

JOURNAL Genomics 71 (2), 200-213 (2001)

MEDLINE 21100893

PUBMED 1161814

REFERENCE 2 (bases 1 to 1606)

AUTHORS Hadano, S., Ikeda, J. and Hayden, M.R.

JOURNAL

Direct Submission
Submitted (24-FEB-2000) Shinji Hadano, Tokai University, The Institute of Medical Sciences, Bohseidai, Isehara, Kanagawa 259-1193, Japan (E-mail: shinji.ena.med.u-tokai.ac.jp, Tel.: +81-463-91-5095, Fax: +81-463-91-4993)

FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Homo sapiens NIF3L1 protein mRNA, complete cds.

ACCESSION AF283538
 VERSION AF283538.1 GI:12006402
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 REFERENCE 1 (bases 1 to 1425)
 Tascou, S., Uedelhoven, J., Dixkens, C., Neyerla, K., Engel, W. and Burelind, P.
 Isolation and characterization of a novel human gene, NIF3L1, and its mouse ortholog, Nif3l1, highly conserved from bacteria to mammals
 TITLE
 JOURNAL CytoGenet. Cell Genet. 90 (3-4), 330-336 (2000)
 MEDLINE 20573864
 PUBMED 11124544
 REFERENCE 2 (bases 1 to 1425)
 Tascou, S., Burelind, P. and Engel, W.
 Direct Submission
 Submitted (29-JUN-2000) Institute for Human Genetics, University of Goettingen, Heinrich-Dueker Weg 12, Goettingen 37073, Germany
 JOURNAL
 TITLE
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 QY 1147 TTCCCAAGGAATTAATGTCATCTCTGTGAACACACACACAGAGAGGCTTCTTTC 1206
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RESULT 5
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 LOCUS
 DEFINITION Homo sapiens, similar to NIF3 (Ngi) interacting factor 3, S. Pombe
 accession BC007654
 homolog-1-like 1, clone MGC:2595 IMAGE:3346099, mRNA, complete cds.
 VERSION BC007654.1 GI:14043316
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1440)
 Strausberg, R.
 Direct Submission
 Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCMP/FTP

CDNA Library Preparation: Rabin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium, (LUNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Bethesda, Maryland;

Web site: http://www.nisc.nih.gov/nisc_mgcenhgt1.nih.gov
Contact: nisc_mgcenhgt1.nih.gov
Shevchenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakespear, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legsall, R., Lim, M., Maduro, O.L., Massello, C., Mastiani, S.D., McCloskey, C., McDowell, J., Pearson, R., Snyder, B., Stantilpop, S., Thomas, P.J., Tlomek, E.E., Touchman, D.W., Tsurguev, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNt at: <http://image.llnl.gov>
Series: IRML Plate: 5 Row: 1 Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 10197631.

FEATURES

source

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Db	60	AGTCCCAACGACATCCGGTTTGAGATTCCTCTGTCGAAATCTCCCGTCCCTCAT	119
QY	247	GGATTGAAGGCTCCCTTCCTTCCTGTAAGATCTTCATCCCTCCGTTGCGAGAG	306
Db	120	GGATTGAAGGCTTCCTTCCTTCCTGTAAGATCTTCATCCCTCTGTTGCGAGAG	179
QY	307	TTGGGACAATGTTGGATTACTGTGGAAACCAAGCCACACATACTGTAAATACACTTT	366
Db	180	TTGGGACAATGTTGGATTACTGTGGAAACCAAGCCACACATACTGTAAATACACTTT	239
QY	367	CCATCAACAATGACCTGAGCTGAGGAAGATGAGAGAGGTGCTGCAAAAGAAAGCGAGCT	426
Db	240	CCATCAACAATGACCTGAGCTGAGGAAGATGAGAGAGGTGCTGCAAAAGAAAGCGAGCT	299
QY	427	CATTCTCTCCATCCATCCGCTATCTTCGACCCATGAAAGGCGAATACCTGGACACATG	486
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OY		667	AGTAGAATTCAAGTTTAAGTACACCCCAAAGACTGGACAAGTCAATGTCTGACATGAANAAG	726
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OY		727	AATTGACGGGTTCCTGTCACTTCCTTTTTTCGTCAGACACGTGGTAATGAGAAACAACACG	786
Db		600	AATTGACGGGTTCCTGTCACTTCCTTTTTTCGTCAGACACGTGGTAATGAGAAACAACACG	659
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Db		660	GATTAAATCTAAATTTGTACTCAGAAGCGCTTTGATGCAGGTGGTAGAATTTCTTCCCGAAA	719
OY		847	CAAACCACTTTATTCAGAAAGACGGAAATTCGTCACTGAGACAGCCTTTCCTTCAATCAC	906
Db		720	CAAACCACTTTATTCAGAAAGACGGAAATTCGTCACTGAGACAGCCTTTCCTTCAATCAC	779
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OY		967	AATAAAAAAGACACCTAAATATCTCATATTCCTTATGACCCCTTGGGGTGGGAGAACCTT	1026
Db		840	AATAAAAAAGACACCTAAATATCTCATATTCCTTATGACCCCTTGGGGTGGGAGAACCTT	899
OY		1027	AGAGTCTCAAGTCAAATCGTGGCCCTGTGTGCTGTGTCTGTGGGAGACAGCTTTCGACAGG	1086
Db		900	AGAGTCTCAAGTCAAATCGTGGCCCTGTGTGCTGTGTCTGTGGGAGACAGCTTTCGACAGG	959
OY		1087	TGTTTGAGGCGTACCTTTACCTCACAGGTGAGATGTCCATCATATFACCTTTGGATGCTGCG	1146
Db		960	TGTTTGAGGCGTACCTTTACCTCACAGGTGAGATGTCCATCATATFACCTTTGGATGCTGCG	1019
OY		1147	TTCCCAAGGAAATAAATGTATCTCCTGTGTGAACACAGACACATGACAGGCTTTCCTTTC	1206
Db		1020	TTCCCAAGGAAATAAATGTATCTCCTGTGTGAACACAGACACATGACAGGCTTTCCTTTC	1079
OY		1207	TGACCTTCGAGATATGCTGGATTTCTCACTTGGAAATTAAGTAAATATTATCCATACAGA	1266
Db		1080	TGACCTTCGAGATATGCTGGATTTCTCACTTGGAAATTAAGTAAATATTATCCATACAGA	1139
OY		1267	GACTGACAGGAGACCCCTTCAGGTGATATATTACAAACATCAGATAACACATTC	1324
Db		1140	GACTGACAGGAGACCCCTTCAGGTGATATATTACAAACATCAGATAACACATTC	1197
RESULT 6				
LOCUS	AF060513		1387 bp mRNA linear PRI 02-JAN-2001	
DEFINITION	Homo sapiens clone 016d06 My018 protein mRNA, complete cds.			
ACCESSION	AF060513			
VERSION	AF060513.1		GI:12001975	
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1387) Mo, Y.M., Xie, Y., Huang, X.Y., Ying, K. and Dai, J.L. Direct Submission Submitted (20-APR-1998) Institute of Genetics, School of Life Science, Fudan University, 220 Handan Rd., Shanghai 200433, P.R.China			
JOURNAL				
FEATURES				
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BASE COUNT      378 a      323 c      309 g      377 t
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Query Match      73.2%: Score 1137; DB 9; Length 1387;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 248 GATTTGAAGGCTCTCTTCTTCTCTTGAATGACTTTCATCCCTCTGCTTGCTGAAGT 307
    |||||
DB 85 GATTTGAAGGCTCTCTTCTTCTCTTGAATGACTTTCATCCCTCTGCTTGCTGAAGT 144
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QY 308 TGGGACAAATGTTGGATTACTGTGTGAACCAAGCCACACATCTGTAAGAACACTTTC 367
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DB 145 TGGGACAAATGTTGGATTACTGTGTGAACCAAGCCACACATCTGTAAGAACACTTTC 204
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QY 368 CTGACCAATGACTGACTGAGAAAGTATGAGAGAGGTGCTGCAAAAAGAGGACAGCTTC 427
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DB 205 CTGACCAATGACTGACTGAGAAAGTATGAGAGAGGTGCTGCAAAAAGAGGACAGCTTC 264
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QY 428 ATTCTCTCTACCATCCGCTTCTCTCCGACCCATGAAGGCGATTAACCTGGAACACATGG 487
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DB 265 ATTCTCTCTACCATCCGCTTCTCTCCGACCCATGAAGGCGATTAACCTGGAACACATGG 324
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QY 488 AAGGACGCGCTGGTGTATCCGGGCTGTGAGAACAGAGTGGTATCTCTCCCATACA 547
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DB 325 AAGGACGCGCTGGTGTATCCGGGCTGTGAGAACAGAGTGGTATCTCTCCCATACA 384
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QY 548 GCCTATGATGCTGCGGCCAGGCGCTCAACAACTGTTGGCTAAAGGGCTTGGAGCTTGT 607
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QY 668 GTGAAATTCACGTTAACTACACCAAGACCTGGACAAAGTCAATGTCTGAGTGAAGA 727
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QY 848 AATCACTTATATGAGAAAGCGAAATTCCTCAGTGAAGAGCTTTCCTTCACTACT 907
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DB 1045 GACCTTCGATATGCTGATGCTGATTCATCTGAGAAATTAATTAATTCATATCAGAG 1104
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RESULT 7
AX119075
LOCUS
DEFINITION
Sequence 239 from Patent WO0129221.
AX119075
VERSION
AX119075.1 GI:14036029
KEYWORDS
SOURCE
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ORGANISM

REFERENCE
1
Conklin,D.C. and Yee,D.P.
Proteins and polynucleotides encoding them
Patent: WO 0129221-A 239 26-APR-2001;
Zymogenetics, Inc. (US)
JOURNAL
Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1053; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	425	CTCATCTCTCTACCAATCCGCTATCTTCCGACCCATGAGGCGATTAACCTGGAACACA	484
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QY	485	TGGAAGAGGCGCTGTGATCCGGGCTCTGAGAACAGATCGGTATCTCTCTCAT	544
DB	241	TGGAAGAGGCGCTGTGATCCGGGCTCTGAGAACAGATCGGTATCTCTCTCAT	300
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DB	301	ACAGCCATGATGCTGGGCGGCGGCTCAACAACTGGTGTAAAGGCTTGAGCT	360
QY	605	TGTACCTCCAGGCGCATACATCTTCCAAAGCTCCCAACTACCTACAGAGGGAACAC	664
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QY	1265	GAGACTGACAGGAGCCCTCTCAGGTGATATA	1297
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RESULT 8
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 LOCUS
 DEFINITION Homo sapiens mRNA; cDNA DKFp762L015 (from clone DKFp762L015).

QY	298	TGCTGAGAGTGGGCAATGTTGATTAATCTGTTGGAACCAAGCCACCATCTACTTAA	357
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QY	418	GACAGACCTCAATCTCTCTCAACATCCGCTATCTTCCGACCATGAAGCGCATTAACCTG	477
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QY	658	AAACACGAGTAGAATTCACAGTTAACTACACCCAGAGCTGACCAAGATCATGTCTGC	717
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ACCESSION AL834430
 VERSION AL834430.1 GI:21740154
 KEYWORDS
 SOURCE
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1353)
 REFERENCES
 AUTHORS Bloecher, H., Boecher, M., Brandt, P., Mewes, H.W., Well, B. and Wiemann, S.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUL-2002) 1. D-85764 Neuherberg, GERMANY
 COMMENT Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; Brunschwelg/Germany) within the cDNA sequencing consortium of the German Genome Project.
 This clone (DKFZp762L015) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcententrum, Neuherberg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cdna/>.
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 Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 541 TTCCCGGAACAAACACTTATCAGAGAGAGAAATTTCTGCTACGTGAGAGACCTTTGCT 600
QY 898 TCTACACTAGTGAATGGAGGCTTATGACACAGTGAATGCTGCTCCCTGGACACCAT 957
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Db 601 TCTACACTAGTGAATGGAGGCTTATGACACAGTGAATGCTGCTCCCTGGACACCAT 660
QY 958 GATTGATGCAATTAATAAGACACCTTAATCTCATATTCGCTTAGCCCTTGCGGTGGG 1017
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Db 661 GATTGATGCAATTAATAAGACACCTTAATCTCATATTCGCTTAGCCCTTGCGGTGGG 720
QY 1018 GAGAACCTTAGTCTCAAGTCAAAATCCGTGGCCCTGTGCTGCTTCTGGGAGCAGCT 1077
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Db 721 GAGAACCTTAGTCTCAAGTCAAAATCCGTGGCCCTGTGCTGCTTCTGGGAGCAGCT 780
QY 1078 TCTGACAGGCTGTGAGGCTGACCTTACCTACAGGTGAGATGCTCCATCATGATCTTT 1137
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Db 781 TCTGACAGGCTGTGAGGCTGACCTTACCTACAGGTGAGATGCTCCATCATGATCTTT 840
QY 1138 GGATGCTGCTTCCCAAGAAATATGCTCATCTCTGTGAACACAGCAACACTGAGAGG 1197
|||||
Db 841 GGATGCTGCTTCCCAAGAAATATGCTCATCTCTGTGAACACAGCAACACTGAGAGG 900
QY 1198 CTTTCTTTCTGACCTTCGAGATATGCTGATTTCTCACTTGGAGAAATGAGAAATTTAT 1257
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Db 901 CTTTCTTTCTGACCTTCGAGATATGCTGATTTCTCACTTGGAGAAATGAGAAATTTAT 960
QY 1258 CCTATGAGAGCTGACAGGAGCCCTTCAAGTGTGATTAATGACAGAAACATGAGATA 1317
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Db 961 CCTATGAGAGCTGACAGGAGCCCTTCAAGTGTGATTAATGACAGAAACATGAGATA 1020
QY 1318 CACATTC 1324
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Db 1021 CACATTC 1027

RESULT 9
AF182416 1579 bp mRNA linear PRI 20-SEP-2000
LOCUS Homo sapiens MDS015 (MDS015) mRNA, complete cds.
DEFINITION AF182416
ACCESSION AF182416
VERSION AF182416.1 GI:10197631
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Huang, C., Qian, B., Tu, Y., Gu, W., Wang, Y., Han, Z. and Chen, Z.
TITLE Novel genes expressed in hematopoietic stem/progenitor cells from
Myelodysplastic Syndromes patient
JOURNAL
AUTHORS Huang, C., Qian, B., Tu, Y., Gu, W., Wang, Y., Han, Z. and Chen, Z.
TITLE Direct Submision
SUBMITTED (02-SEP-1999) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, People's Republic of China

FEATURES
source

1. .1579
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="hematopoietic stem/progenitor cells"
/note="Isolated from a Myelodysplastic Syndrome patient"
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/gene="MDS015"
244. .1299
CDs
gene
CDs

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KGDIVSVTSFSASRNEOTRINLNCOTKAMOVDPILSRNOLYOKRELLISERPL
AYDAAPQVNNMLAKGLAGCTSRPIHPSKAPNYPTGNGHREVENVYTOTDLKMSAV
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/protein_id="AA014952.1"
/product="MDS015"
/codon_start=1
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Best Local Similarity 99.68; Pred. No. 0;
Matches 1322; Conservative 0; Mismatches 1; Indels 4; Gaps 3;
QY 1 GTGATTGTATCTTGTGCTGTCAGAGACAGCAGAGAGAGATTTGGTCAGAAAACCTGC 60
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Db 1 GTGATTGTATCTTGTGCTGTCAGAGACAGCAGAGAGAGATTTGGTCAGAAAACCTGC 60
QY 61 CCGCCGACACAGACAGCAGCAGTATGAGGAGACAGGAGCTGACTCAGACTTAACCTGG 120
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Db 61 CCGCCGACACAGACAGCAGCAGTATGAGGAGACAGGAGCTGACTCAGACTTAACCTGG 120
QY 121 CTGTGCTGCTGGTTTTCACCTGCTCGGAAAAAGGCTGAAGTGGCAGCTAAATGAGGCA 180
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Db 121 CTGTGT-TCGTGTTTTCACCTGCTCGGAAAAAGGCTGAAGTGGCAGCTAAATGAGGCA 179
QY 181 TAGATGAGTCCCGACGACGACGAGTCCGGTTTGTAGATCCCTGATGCAATCTCCCGTTG 240
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Db 180 TAGATGAGTCCCGACGACGACGAGTCCGGTTTGTAGATCCCTGATGCAATCTCCCGTTG 229
QY 241 CTTATGAGATTTGAAGGCTCTCTTCTTCTTCTTGAATGACTTTGATCCCTCGTTTGC 300
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QY 301 TGAAGTGTGGGACAAATGTTGATTTACTGGTGTGAACCAAGCCACCATATCTGTAATAC 360
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QY 480 ACACATGG--AAGAGAGGCTGTGATCCGGGCTGTGAGAACAGATCGGTATCTACTC 537
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QY 538 TCTCATACAGCTATGATGCTGCGCCGAGGAGGCTCAAACTGTTGGCTAAAGGCT 597
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Db 540 TCTCATACAGCTATGATGCTGCGCCGAGGAGGCTCAAACTGTTGGCTAAAGGCT 599
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QY 718 AGTGAAGGATTTGAGGCTTCTGCTACTTTTCTGCTGAGAGCTGCTAATAGGA 777
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Db 720 AGTGAAGGATTTGAGGCTTCTGCTACTTTTCTGCTGAGAGCTGCTAATAGGA 779
QY 778 ACAACACGATTAATCTGAATTTGACTCAGAGGCTTTGATGACAGGTGGTAGATTTCT 837
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[illegible]

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Similarity	100.0%; Pred. No. 2.8e-269; Indels 0; Gaps 0;
Matches	567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GTGATTTGTATTCTTGGTGCTGCAGAGGACAGCAGAAGAGGATTTGGGTCAAAAAGTCG 60
DB	 27 GTGATTTGTATTCTTGGTGCTGCAGAGGACAGCAGAAGAGGATTTGGGTCAAAAAGTCG 86
QY	61 CCTCCCGCACAGACAGCAGCGCACTAGTGGGAAGAGGGTCCATCAGACTTAACGTG 120
DB	 87 CCTCCCGCACAGACAGCAGCGCACTAGTGGGAAGAGGGTCCATCAGACTTAACGTG 146
QY	121 CTGTGTCTCGTGTGTTTTTCACTGCTCTGGAAAAAGCGCTGAAGTGGCACTGAAATAGAGCA 180
DB	 147 CTGTGTCTCGTGTGTTTTTCACTGCTCTGGAAAAAGCGCTGAAGTGGCACTGAAATAGAGCA 206
QY	181 TAGATGAGTCCCCACAGACAGTCCGGTTGTGTGATTCCTGTATCTGCAATTCCTCCGCTTC 240
DB	 207 TAGATGAGTCCCCACAGACAGTCCGGTTGTGTGATTCCTGTATCTGCAATTCCTCCGCTTC 266
QY	241 CTTGATGATTTTGAAGGCGTCTCTCTTCTCTCTTAAATGACTTTTCATCCCTCTCGTTGTC 300
DB	 267 CTTGATGATTTTGAAGGCGTCTCTCTTCTCTCTTAAATGACTTTTCATCCCTCTCGTTGTC 326
QY	301 TGAGAGTTGGGACAATGTTGGATTACTGTGTGGAACCAAGCCCACCACATTACTGTAAATAC 360
DB	 327 TGAGAGTTGGGACAATGTTGGATTACTGTGTGGAACCAAGCCCACCACATTACTGTAAATAC 386
QY	361 ACTCTTCCTGACCATGACTGACTGAGGAAGTATGAGGAGGTGTCGCAAAAAGAAAGC 420
DB	 387 ACTCTTCCTGACCATGACTGACTGAGGAAGTATGAGGAGGTGTCGCAAAAAGAAAGC 446
QY	421 AGACCTCATTTCTCTCTACCATCCGCCCTATCTTCCGACCATGAAGCGGCATTAACCTGGAA 480
DB	 447 AGACCTCATTTCTCTCTACCATCCGCCCTATCTTCCGACCATGAAGCGGCATTAACCTGGAA 506
QY	481 CACATGGAAGAGGCGCTGTGTGATCCGGGCTCTGGAGAACAGAGTCGTATCTACTCTCC 540
DB	 507 CACATGGAAGAGGCGCTGTGTGATCCGGGCTCTGGAGAACAGAGTCGTATCTACTCTCC 566
QY	541 TCATACAGCCTATGATGCTGGCCCCA 567
DB	 567 TCATACAGCCTATGATGCTGGCCCCA 593
RESULT 11	
LOCUS	AC037455/c
DEFINITION	Homo sapiens chromosome 02 clone RP11-422L5, WORKING DRAFT
ACCESSION	AC037455
VERSION	AC037455.5 GI:9887641
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 170586)
AUTHORS	Smith,D.R.
TITLE	Genome Therapeutics Corporation Sequencing Center: Human Genome Sequence Data
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 170586)
AUTHORS	Smith,D.R.
TITLE	Direct Submission
JOURNAL	Submitted (09-Apr-2000) Genome therapeutics Corporation, 100 Beaver

COMMENT

Street, Waltham, MA 02453, USA
On Aug 24, 2000 this sequence version replaced gi:8569072.

Genome Center

Center: Genome Therapeutics Corporation

Center code: GTC

Web site: <http://www.genomecorp.com/>

Contact: gtc-seqcenter@genomecorp.com

Project information

Center project name: hg215

Summary Statistics

Sequencing vector: N/A

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 990315

Consensus quality: 147001 bases at least Q40

Consensus quality: 157396 bases at least Q30

Consensus quality: 159713 bases at least Q20

Insert size: 168303; sum-of-contigs

Quality coverage: 3.8x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1171: contig of 1171 bp in length
1172 1271: gap of unknown length
1272 2319: contig of 1048 bp in length
2320 2419: gap of unknown length
2420 3793: contig of 1374 bp in length
3794 3893: gap of unknown length
3894 5414: contig of 1521 bp in length
5415 5514: gap of unknown length
5515 8773: contig of 3259 bp in length
8774 10904: contig of 2031 bp in length
10905 11004: gap of unknown length
11005 13204: contig of 2200 bp in length
13205 13304: gap of unknown length
13305 16401: contig of 3097 bp in length
16402 16501: gap of unknown length
16502 18227: contig of 1726 bp in length
18228 18327: gap of unknown length
18329 22401: contig of 4074 bp in length
22402 22501: gap of unknown length
22502 25177: contig of 2676 bp in length
25178 25277: gap of unknown length
25278 29892: contig of 4615 bp in length
29893 29992: gap of unknown length
29993 33457: contig of 3465 bp in length
33458 33557: gap of unknown length
33558 37405: contig of 3848 bp in length
37406 37505: gap of unknown length
37506 41734: contig of 4229 bp in length
41735 41834: gap of unknown length
41835 48989: contig of 7165 bp in length
48990 49099: gap of unknown length
49000 56076: contig of 6977 bp in length
56077 56176: gap of unknown length
56177 63604: contig of 7428 bp in length
63605 63704: gap of unknown length
63705 70821: contig of 7117 bp in length
70822 70921: gap of unknown length
70922 80138: contig of 9217 bp in length
80139 80238: gap of unknown length
80239 88780: contig of 8542 bp in length
88781 88880: gap of unknown length
88881 104642: contig of 15762 bp in length
104643 104742: gap of unknown length
104743 124656: contig of 19914 bp in length
124657 124756: gap of unknown length

* 124757 143891: contig of 19135 bp in length
* 143892 143991: gap of unknown length
* 143992 170586: contig of 26595 bp in length.
Location/Qualifiers

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/chromosome="02"

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/note="assembly_name:Contig13"

2420. 3793

/note="assembly_name:Contig17"

3894. 5414

/note="assembly_name:Contig18"

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/note="assembly_name:Contig19"

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33558. 37405

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37506. 41734

/note="assembly_name:Contig29"

41835. 48999

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clone_end:SP6

56177. 63604

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63705. 70821

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80239. 88780

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143992. 170586

/note="assembly_name:Contig39"

BASE COUNT 50417 a 34173 c 33290 g 50259 t 2447 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.9e-194;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 AGTCCACACAGCAGTCCGCTTGTAGATTCCTGATCGATCGAATTCCTCCGCTTCAT 246
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Db 140127 AGTCCACACACAGCAGTCCGCTTGTAGATTCCTGATCGAATTCCTCCGCTTCAT 140068

OY 247 GGATTGAAGGCTCTCTTCTTCTTGAATGACTTTGCATCCCTCTGTTGTAGAG 306
 DB 140067 GGAATTGAAGGCTCTCTTCTTCTTGAATGACTTTGCATCCCTCTGTTGTAGAG 140008
 OY 307 TTGGACAATGTTGATACGTGAGGAGCAAGCCACACATANTGTAAATACACTCT 366
 DB 140007 TTGGACAATGTTGATACGTGAGGAGCAAGCCACACATANTGTAAATACACTCT 139948
 OY 367 CCTGACCAATGACCTGACTGAGGAGAGTATGAGAGAGGTGCTGCAAAAGAGGAGACT 426
 DB 139947 CCTGACCAATGACCTGACTGAGGAGAGTATGAGAGAGGTGCTGCAAAAGAGGAGACT 139888
 OY 427 CATCTCTCTTACCATCCGCTATCTTCCGACCATGAGAGGCATACCTGGACACATG 486
 DB 139887 CATCTCTCTTACCATCCGCTATCTTCCGACCATGAGAGGCATACCTGGACACATG 139828
 OY 487 GAAGGAGGCGCTGGATGAGGCGGCTGAGAGAGAGTATCTACTCTCTCATAC 546
 DB 139827 GAAGGAGGCGCTGGATGAGGCGGCTGAGAGAGAGTATCTACTCTCTCATAC 139768
 OY 547 AGCCTATGATCTGGCGCCCAAGGCGTCAACACTGTTGGCTAAAGGCTTGG 600
 DB 139767 AGCCTATGATCTGGCGCCCAAGGCGTCAACACTGTTGGCTAAAGGCTTGG 139714
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 VERSION AC005037.2 GI:4827310
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074
 REFERENCE
 AUTHORS 2 (bases 1 to 190508)
 TITLE Abbot, A. and Le, T.
 JOURNAL The sequence of Homo sapiens BAC clone RP11-469M7
 REFERENCE
 AUTHORS 3 (bases 1 to 190508)
 TITLE Unpublished
 JOURNAL Waterston, R.H.
 REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (12-JUN-1998) Genome Sequencing Center, Washington
 JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 AUTHORS 4 (bases 1 to 190508)
 TITLE Waterston, R.H.
 JOURNAL Direct Submission
 TITLE Submitted (14-MAY-1999) Genome Sequencing Center, Washington
 JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 REFERENCE
 AUTHORS 5 (bases 1 to 190508)
 TITLE Waterston, R.
 JOURNAL Direct Submission
 TITLE Submitted (30-SEP-2000) Department of Genetics, Washington
 JOURNAL University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On May 14, 1999 this sequence version replaced g1:3309089.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: saplens@wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0469M07

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPc1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tateo, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)
 VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1308; the clone sequenced to the right is RP11-91M5. Actual start of this clone is at base position 1 of RP11-469M7; actual end is at 190508 of RP11-469M7.

FEATURES

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 5545..5585
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 5586..5873
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 5876..6007
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[illegible]

Center project name: H_NH0663N02

* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1912: contig of 1912 bp in length
* 1913 2012: gap of unknown length
* 2013 3539: contig of 1527 bp in length
* 3540 3639: gap of unknown length
* 3640 6127: contig of 2488 bp in length
* 6128 6227: gap of unknown length
* 6228 9244: contig of 3017 bp in length
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* 13289 13389: gap of unknown length
* 13389 16301: contig of 2913 bp in length
* 16302 16401: gap of unknown length
* 16402 20096: contig of 3695 bp in length
* 20097 20196: gap of unknown length
* 20197 24467: contig of 4271 bp in length
* 24468 24567: gap of unknown length
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* 32595 35626: contig of 3032 bp in length
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* 40051 40150: gap of unknown length
* 40151 43881: contig of 3731 bp in length
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* 43982 50194: contig of 6213 bp in length
* 50195 50294: gap of unknown length
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* 64761 72159: contig of 7399 bp in length
* 72160 72259: gap of unknown length
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* 79836 79935: gap of unknown length
* 79936 90863: contig of 10928 bp in length
* 90864 90963: gap of unknown length
* 90964 99401: contig of 8437 bp in length
* 99401 99500: gap of unknown length
* 99501 114190: contig of 14690 bp in length
* 114191 114290: gap of unknown length
* 114291 127822: contig of 13532 bp in length
* 127823 127922: gap of unknown length
* 127923 143474: contig of 15552 bp in length
* 143475 143574: gap of unknown length
* 143575 170444: contig of 26870 bp in length
* 170445 170544: gap of unknown length
* 170545 195651: contig of 25107 bp in length
* 195652 195751: gap of unknown length
* 195752 198250: contig of 2499 bp in length.

FEATURES

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	43982. 50194	
	misc_feature	/note="assembly_name:Contig23"
	50295. 57454	
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	57555. 64660	
	misc_feature	/note="assembly_name:Contig25"
	64761. 72159	
	misc_feature	/note="assembly_name:Contig26"
	72260. 79835	
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	79936. 90863	
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	Matches 414; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	187 AGTCCCGACGACGCGGTTGTGATTCCTGATCTGCAATTTCCCGTCTTCAT	246
DB	14089 AGTCCCGACGACGCGGTTGTGATTCCTGATCTGCAATTTCCCGTCTTCAT	14148
QY	247 GGAATTTGAAGGCTCTCTCTCTCTCTCTGATGATCTTCGATCCCTGCTTGAGAG	306
DB	14149 GGAATTTGAAGGCTCTCTCTCTCTCTCTGATGATCTTCGATCCCTGCTTGAGAG	14208
QY	307 TTGGGACATGTTGGATTACTGTTGGAACGACCCACACATCTGTAATACACTCTT	366
DB	14209 TTGGGACATGTTGGATTACTGTTGGAACGACCCACACATCTGTAATACACTCTT	14268
QY	367 CCTGACCAATGACTGCTGAGGAAGTGTGAGGAGGCTGCTGCAAAAAGAGGAGACT	426
DB	14269 CCTGACCAATGACTGCTGAGGAAGTGTGAGGAGGCTGCTGCAAAAAGAGGAGACT	14328
QY	427 CATTCCTGCAATGCGGCTATCTCGACCCGATGAGGCGCATTAACCTGGAACATG	486
DB	14329 CATTCCTGCAATGCGGCTATCTCGACCCGATGAGGCGCATTAACCTGGAACATG	14388

QY 487 GAAGAGCGCGTGTGATCCGGGCTCTGGAGAACAGTGGTATCTACTCTCCCTATAC 546
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DB 14389 GAAGAGCGCGTGTGATCCGGGCTCTGGAGAACAGTGGTATCTACTCTCCCTATAC 14448
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QY 547 ACCCTATGATGCTGGCGCCAGGCGCTCAACAACACTGGTGAAGGCGCTTG 600
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DB 14449 ACCCTATGATGCTGGCGCCAGGCGCTCAACAACACTGGTGAAGGCGCTTG 14502
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RESULT 14
BD049005 249 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD049005
VERSION BD049005.1 GI:22590747
KEYWORDS JP 2001269182-A/25251.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 249)
AUTHORS Edwards,J.B.D.M., Duclat,E. and Jordan,J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 25251 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/25251
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCIAT, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68, G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
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FH Key Location/Qualifiers.
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/organism="Homo sapiens"
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Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 272 TTGAATGACCTTCGATCCCTCTGTTGCTGAGAGTTGGACAATGTTGATTAAGTG 331
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DB 37 TTGAATGACCTTCGATCCCTCTGTTGCTGAGAGTTGGACAATGTTGATTAAGTG 96
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QY 332 GAACCAAGCCACACATACCTGTAATACACTCTCTGACCAATGACCTGAGAGAA 391
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DB 97 GAACCAAGCCACACATACCTGTAATACACTCTCTGACCAATGACCTGAGAGAA 156
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QY 392 GTGATGAGAGAGTGTGCAAAAAGAGAGACCTATTCTCTCAACATCCGCTATC 451
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DB 157 GTGATGAGAGAGTGTGCAAAAAGAGAGACCTATTCTCTCAACATCCGCTATC 216
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QY 452 TTCCGACCATGAAGGCGATACCTGGAAC 481
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DB 217 TTCCGACCATGAAGGCGATACCTGGAAC 246
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LOCUS
DEFINITION Homo sapiens chromosome 4 clone RP11-663N2, *** SEQUENCING IN
PROGRESS ***, 26 unordered pieces.

ACCESSION AC093681
VERSION AC093681.2 GI:15987253
KEYWORDS HTG; HTGS_PHASE1
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 198250)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 198250)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Oct 9, 2001 this sequence version replaced gi:15487524.
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@wustl.wustl.edu
----- Project Information -----
Center project name: H.NH0663N02
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1912: contig of 1912 bp in length
* 1913 2012: gap of unknown length
* 2013 3539: contig of 1527 bp in length
* 3540 3639: gap of unknown length
* 3640 6127: contig of 2488 bp in length
* 6128 6227: gap of unknown length
* 6228 9244: contig of 3017 bp in length
* 9245 9344: gap of unknown length
* 9344 13288: contig of 3944 bp in length
* 13289 13388: gap of unknown length
* 13389 16301: contig of 2913 bp in length
* 16302 16401: gap of unknown length
* 16402 20096: contig of 3695 bp in length
* 20097 20197: gap of unknown length
* 20197 24467: contig of 4271 bp in length
* 24468 24567: gap of unknown length
* 24568 28680: contig of 4113 bp in length
* 28681 28780: gap of unknown length
* 28781 32494: contig of 3714 bp in length
* 32495 32595: gap of unknown length
* 32595 35626: contig of 3032 bp in length
* 35627 35726: gap of unknown length
* 35727 40050: contig of 4324 bp in length
* 40051 40150: gap of unknown length
* 40151 43881: contig of 3731 bp in length
* 43882 43981: gap of unknown length
* 43982 50194: contig of 6213 bp in length
* 50195 50294: gap of unknown length
* 50295 57454: contig of 7160 bp in length
* 57455 57554: gap of unknown length
* 57555 64660: contig of 7106 bp in length
* 64661 72159: contig of 7399 bp in length
* 72160 72259: gap of unknown length
* 72260 79835: gap of 7576 bp in length
* 79836 79935: contig of unknown length
* 79936 90863: contig of 10928 bp in length
* 90864 gap of unknown length

*	90964	99400:	contig of 8437 bp in length
*	99401	99500:	gap of unknown length
*	99501	114190:	contig of 14690 bp in length
*	114191	114290:	gap of unknown length
*	114291	127822:	contig of 13332 bp in length
*	127823	127922:	gap of unknown length
*	127923	143474:	contig of 15552 bp in length
*	134475	143574:	gap of unknown length
*	143575	170444:	contig of 26870 bp in length
*	170445	170544:	gap of unknown length
*	170545	195651:	contig of 25107 bp in length
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*	195752	198250:	contig of 2439 bp in length

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FEATURES
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/chromosome="4"
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99501. .114190
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170545. .195651
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195752. .198250
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BASE COUNT 56011 a 43355 c 41444 g 55928 t 2512 others

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ORIGIN

Query Match	9.1%;	Score 141;	DB 2;	Length 198250;
Best Local Similarity	100.0%;	Pred. No. 1.2e-58;		
Matches 141;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	888	AGCCTTTGCTTACATACATCGGAATGGAGGTTATGCAACATCGGATGTAATCGTCCG	947
Db	10961	AGCCTTTGCTTACATACATCGGAATGGAGGTTATGCAACATCGGATGTAATCGTCCG	10902
QY	948	TGGCAACCATGATGTGATCGAATAAAAAGACACCTAAACATATCTATATTCGCTTAGCCC	1007
Db	10901	TGGCAACCATGATGTGATCGAATAAAAAGACACCTAAACATATCTATATTCGCTTAGCCC	10842
QY	1008	TTGGGGTGGGAGAACCTTAG	1028
Db	10841	TTGGGGTGGGAGAACCTTAG	10821

Search completed: August 23, 2003, 16:41:11
Job time : 3963 secs